(FILE 'HOME' ENTERED AT 08:54:47 ON 01 DEC 2003)

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 08:54:50 ON 01 DEC 2003

L1 55 S RPN11
L2 33 S L1 AND UBIQUITIN
L3 18 DUP REM L2 (15 DUPLICATES REMOVED)
L4 4 S L3 AND SIC1

FILE 'STNGUIDE' ENTERED AT 08:56:16 ON 01 DEC 2003

FILE 'MEDLINE, CAPLUS, BIOSIS, AGRICOLA' ENTERED AT 08:59:52 ON 01 DEC 2003

L5 29 DUP REM L1 (26 DUPLICATES REMOVED)
L6 4 S L5 AND (INHIBIT? OR MODIFY?)
L7 133 S SIC1 AND UBIQUITIN
L8 68 DUP REM L7 (65 DUPLICATES REMOVED)
L9 659 S CULLIN AND UBIQUITIN
L10 0 S L9 AND CU11
L11 171 S L9 AND CUL1
L12 1 S L1 AND JAB

=> s l1 and jam
L13 1 L1 AND JAM

L3 ANSWER 17 OF 18 MEDLINE on STN DUPLICATE 8
AN 2000414768 MEDLINE
DN 20372738 PubMed ID: 10913188
TI Evidence for separable functions of Srp1p, the yeast homolog of importin alpha (Karyopherin alpha): role for Srp1p and Sts1p in protein degradation.
AU Tabb M M; Tongaonkar P; Vu L; Nomura M
CS Departments of Microbiology and Molecular Genetics and Biological Chemistry, University of California, Irvine, Irvine, California 92697-1700, USA.
NC GM35949 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, (2000 Aug) 20 (16) 6062-73. Journal code: 8109087. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200008
ED Entered STN: 20000907
Last Updated on STN: 20030214
Entered Medline: 20000828
AB Srp1p (importin alpha) functions as the nuclear localization signal (NLS) receptor in Saccharomyces cerevisiae. The srp1-31 mutant is defective in this nuclear localization function, whereas an srp1-49 mutant exhibits defects that are unrelated to this localization function, as was confirmed by intragenic complementation between the two mutants. **RPN11** and STS1 (DBF8) were identified as high-dosage suppressors of the srp1-49 mutation but not of the srp1-31 mutation. We found that Sts1p interacts directly with Srp1p in vitro and also in vivo, as judged by coimmunoprecipitation and two-hybrid analyses. Mutants of Sts1p that cannot interact with Srp1p are incapable of suppressing srp1-49 defects, strongly suggesting that Sts1p functions in a complex with Srp1p. STS1 also interacted with the second suppressor, **RPN11**, a subunit of the 26S proteasome, in the two-hybrid system. Further, degradation of Ub-Pro-beta-galactosidase, a test substrate for the **ubiquitin** -proteasome system, was defective in srp1-49 but not in srp1-31. This defect in protein degradation was alleviated by overexpression of either **RPN11** or STS1 in srp1-49. These results suggest a role for Srp1p in regulation of protein degradation separate from its well-established role as the NLS receptor.

L3 ANSWER 15 OF 18 MEDLINE on STN DUPLICATE 6
AN 2002491539 MEDLINE
DN 22239942 PubMed ID: 12353037
TI A cryptic protease couples deubiquitination and degradation by the proteasome.
CM Comment in: Nature. 2002 Sep 26;419(6905):351-3
AU Yao Tingting; Cohen Robert E
CS Department of Biochemistry, University of Iowa, 51 Newton Road, Iowa City, Iowa 52242, USA.
SO NATURE, (2002 Sep 26) 419 (6905) 403-7.
Journal code: 0410462. ISSN: 0028-0836.
CY England: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200210
ED Entered STN: 20020928
Last Updated on STN: 20021031
Entered Medline: 20021018
AB The 26S proteasome is responsible for most intracellular proteolysis in eukaryotes. Efficient substrate recognition relies on conjugation of substrates with multiple **ubiquitin** molecules and recognition of the polyubiquitin moiety by the 19S regulatory complex--a multisubunit assembly that is bound to either end of the cylindrical 20S proteasome core. Only unfolded proteins can pass through narrow axial channels into the central proteolytic chamber of the 20S core, so the attached polyubiquitin chain must be released to allow full translocation of the substrate polypeptide. Whereas unfolding is rate-limiting for the degradation of some substrates and appears to involve chaperone-like activities associated with the proteasome, the importance and mechanism of degradation-associated deubiquitination has remained unclear. Here we report that the POH1 (also known as **Rpn11** in yeast) subunit of the 19S complex is responsible for substrate deubiquitination during proteasomal degradation. The inability to remove **ubiquitin** can be rate-limiting for degradation in vitro and is lethal to yeast. Unlike all other known deubiquitinating enzymes (DUBs) that are cysteine proteases, POH1 appears to be a Zn(2+)-dependent protease.

1: Mol Cell. 2001 Aug;8(2):439-48. Related Articles, Links

Cell Press

Selective degradation of ubiquitinated Sic1 by purified 26S proteasome yields active S phase cyclin-Cdk.

Verma R, McDonald H, Yates JR 3rd, Deshaies RJ.

Howard Hughes Medical Institute, Division of Biology, California Institute of Technology, Pasadena, CA 91125, USA.

Selective degradation of single subunits of multimeric complexes by the ubiquitin pathway underlies multiple regulatory switches, including those involving cyclins and Cdk inhibitors. The machinery that segregates ubiquitinated proteins from unmodified partners prior to degradation remains undefined. We report that ubiquitinated Sic1 (Ub-Sic1) embedded within inactive S phase cyclin-Cdk (S-Cdk) complexes was rapidly degraded by purified 26S proteasomes, yielding active S-Cdk. Mutant proteasomes that failed to degrade Ub-Sic1 activated S-Cdk only partially in an ATP-dependent manner. Whereas Ub-Sic1 was degraded within approximately 2 min, spontaneous dissociation of Ub-Sic1 from S-Cdk was approximately 200-fold slower. We propose that the 26S proteasome has the intrinsic capability to extract, unfold, and degrade ubiquitinated proteins while releasing bound partners untouched. Activation of S-Cdk reported herein represents a complete reconstitution of the regulatory switch underlying the G1/S transition in budding yeast.

PMID: 11545745 [PubMed - indexed for MEDLINE]